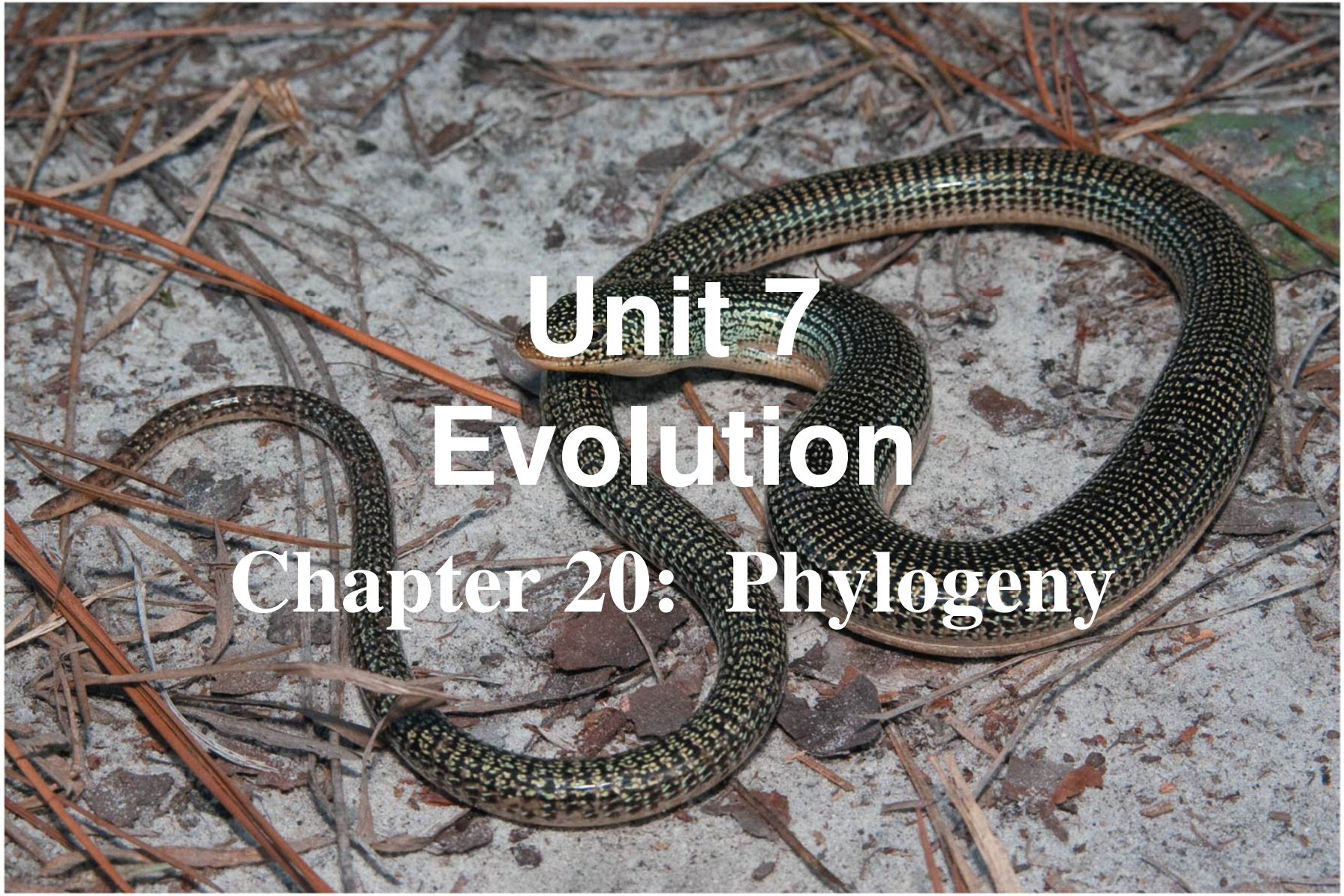
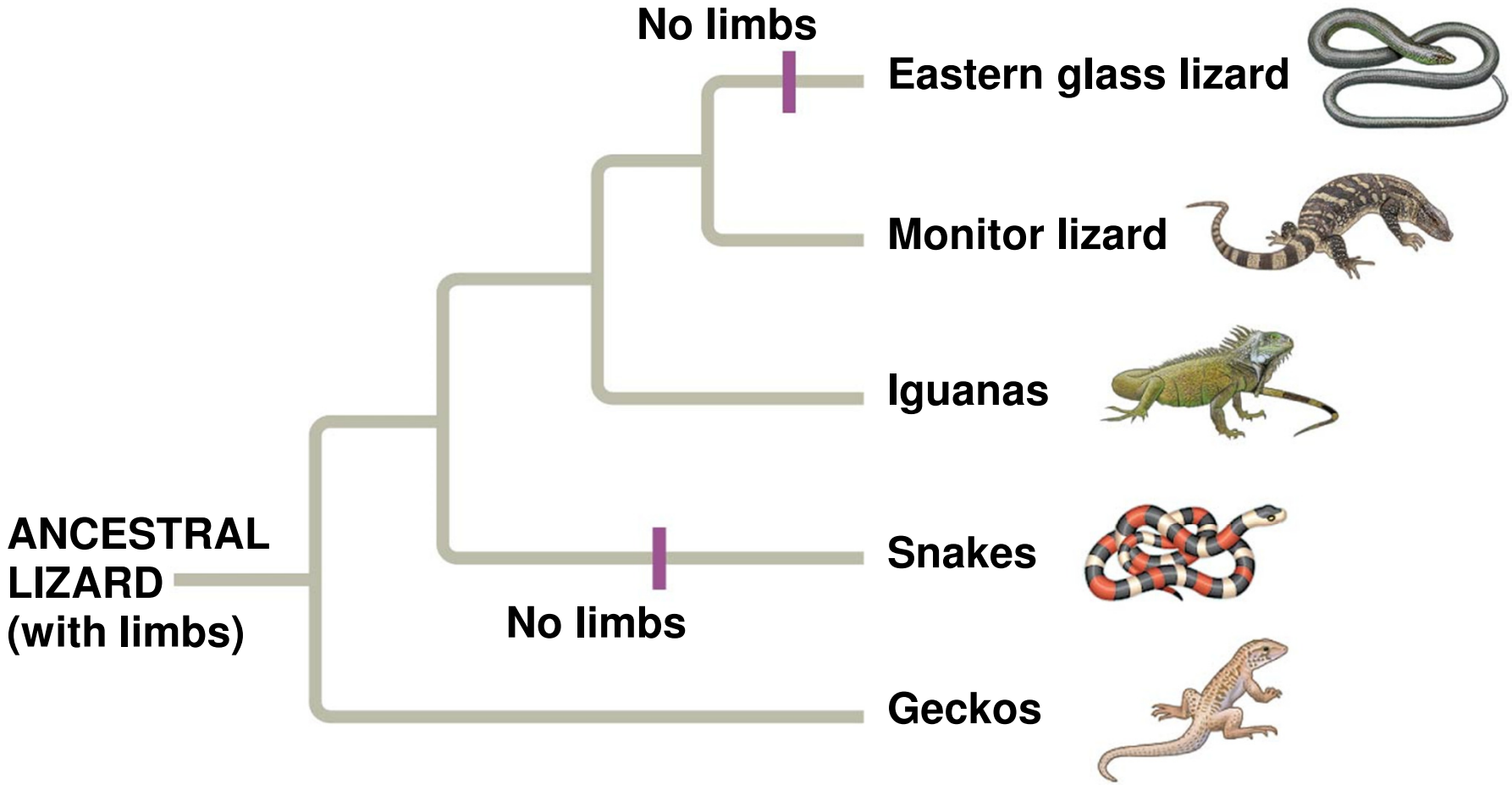


Unit 7
Evolution
Chapter 20: Phylogeny

Overview: Investigating the Evolutionary History of Life

- Legless lizards and snakes evolved from different lineages of lizards with legs
  - Legless lizards have evolved independently in several different groups through adaptation to similar environments
- **Phylogeny** is the evolutionary history of a species or group of related species
- The discipline of **systematics** classifies organisms and determines their evolutionary relationships

Figure 20.2


No limbs
Eastern glass lizard
Monitor lizard
Iguanas
ANCESTRAL LIZARD (with limbs)
Snakes
No limbs
Geckos

Concept 20.1: Phylogenies show evolutionary relationships

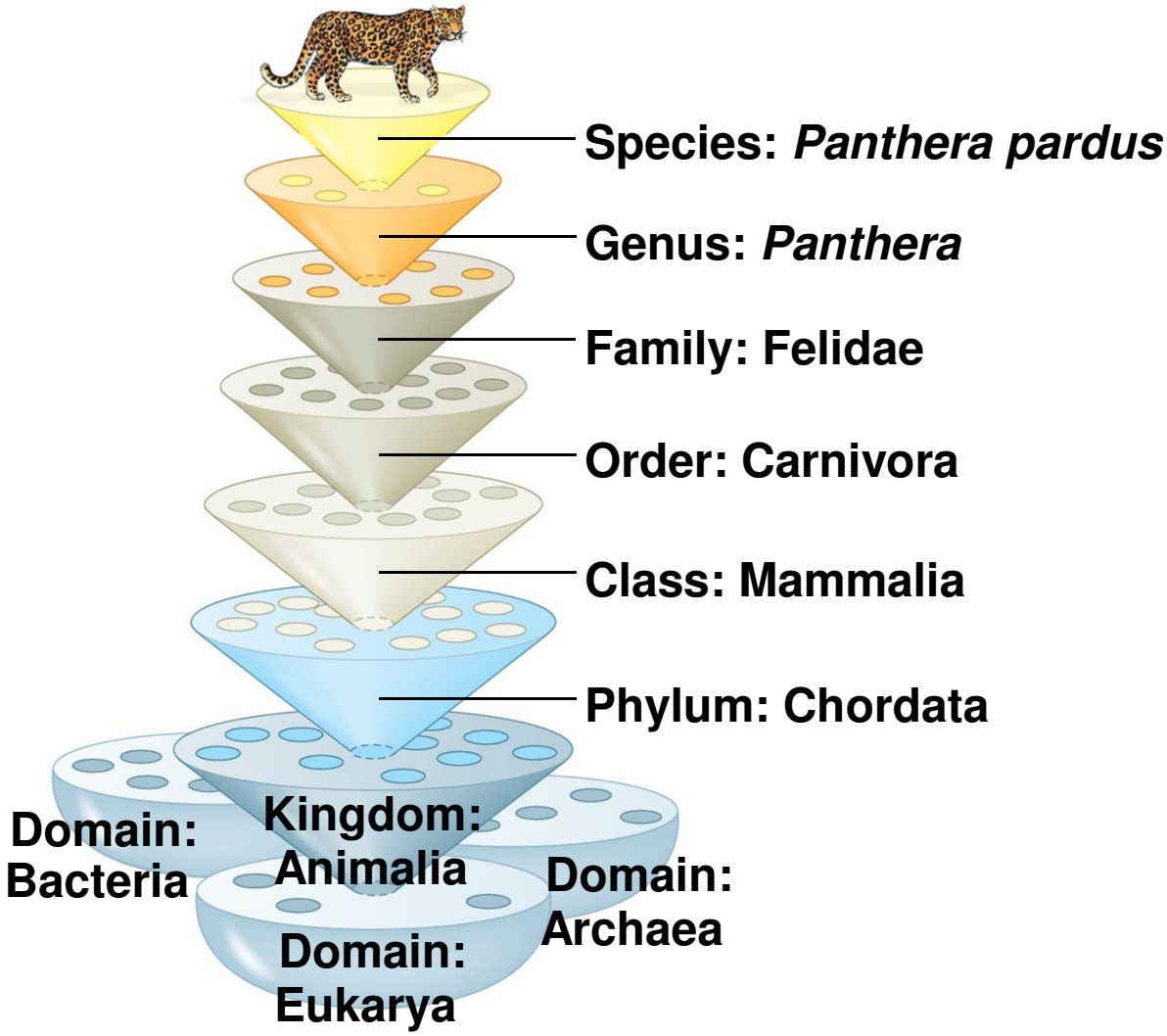
- **Taxonomy** is the discipline of naming and classifying organisms
- In the 18th century, Carolus Linnaeus published a system of taxonomy based on resemblances
- Two key features of his system remain useful today:
  - Two-part names for species
  - Hierarchical classification

Binomial Nomenclature

- The two-part scientific name of a species is called a **binomial**
  - The first part of the name is the **genus**
  - The second part, called the specific epithet, is unique for each species within the genus
- The first letter of the genus is capitalized
- The entire species name is italicized
  - Both parts together name the species (not the specific epithet alone)

Hierarchical Classification

- The taxonomic groups from broad to narrow are
  - Domain
  - Kingdom
  - Phylum
  - Class
  - Order
  - Family
  - Genus
  - Species



- A taxonomic unit at any level of hierarchy is called a **taxon**
  - Ex: Mammalia is a taxon at the class level
- The broader taxa are not comparable between lineages
  - For example, an order of snails has less genetic diversity than an order of mammals

Linking Classification and Phylogeny

- Systematists depict evolutionary relationships in branching **phylogenetic trees**
  - A phylogenetic tree represents a hypothesis about evolutionary relationships
- Each **branch point** represents the divergence of two taxa from a common ancestor
- **Sister taxa** are groups that share an immediate common ancestor

- A **rooted** tree includes a branch to represent the most recent common ancestor of all taxa in the tree
- A **basal taxon** diverges early in the history of a group and originates near the common ancestor of the group
- A **polytomy** is a branch from which more than two groups emerge

Figure 20.4

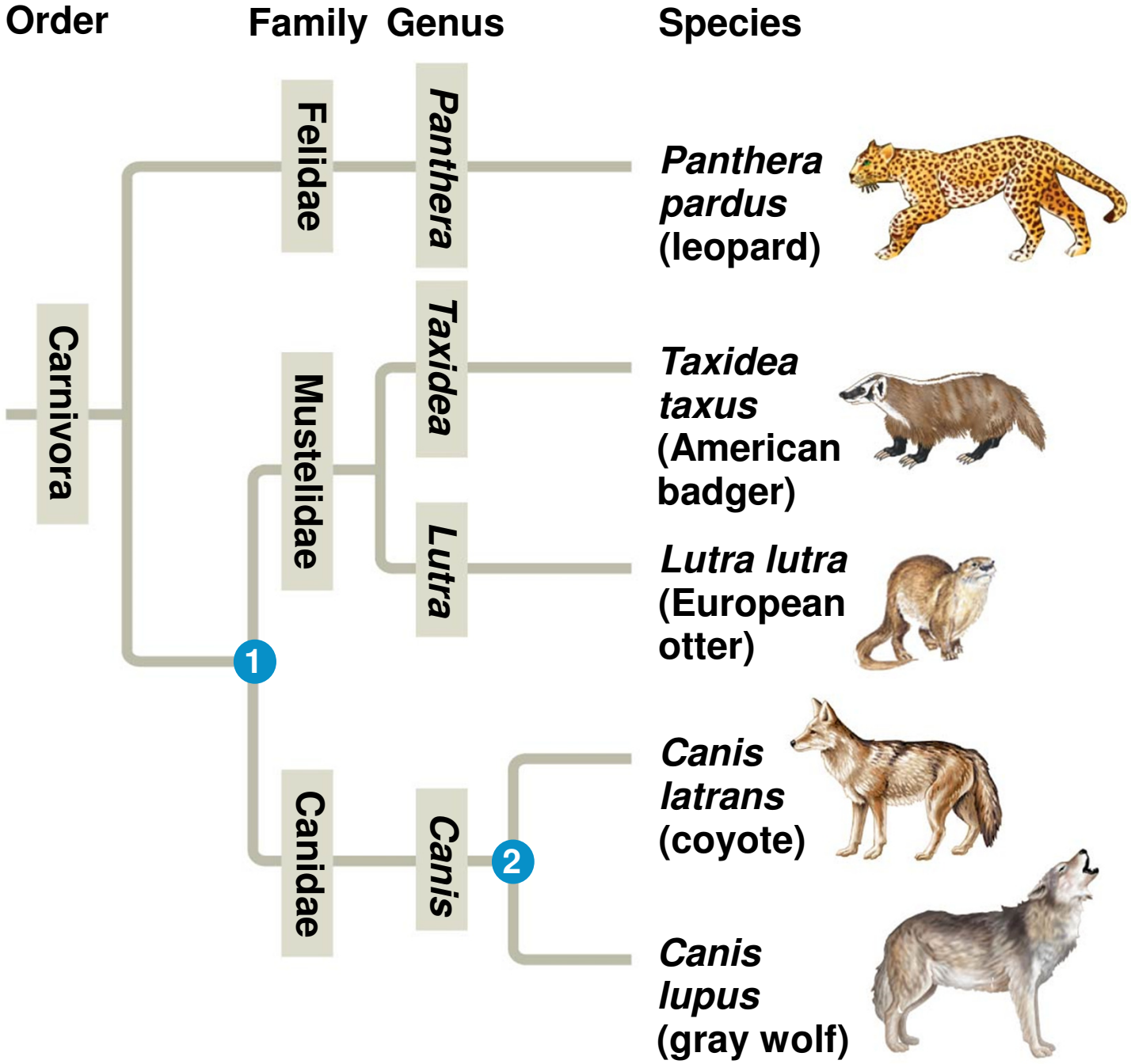
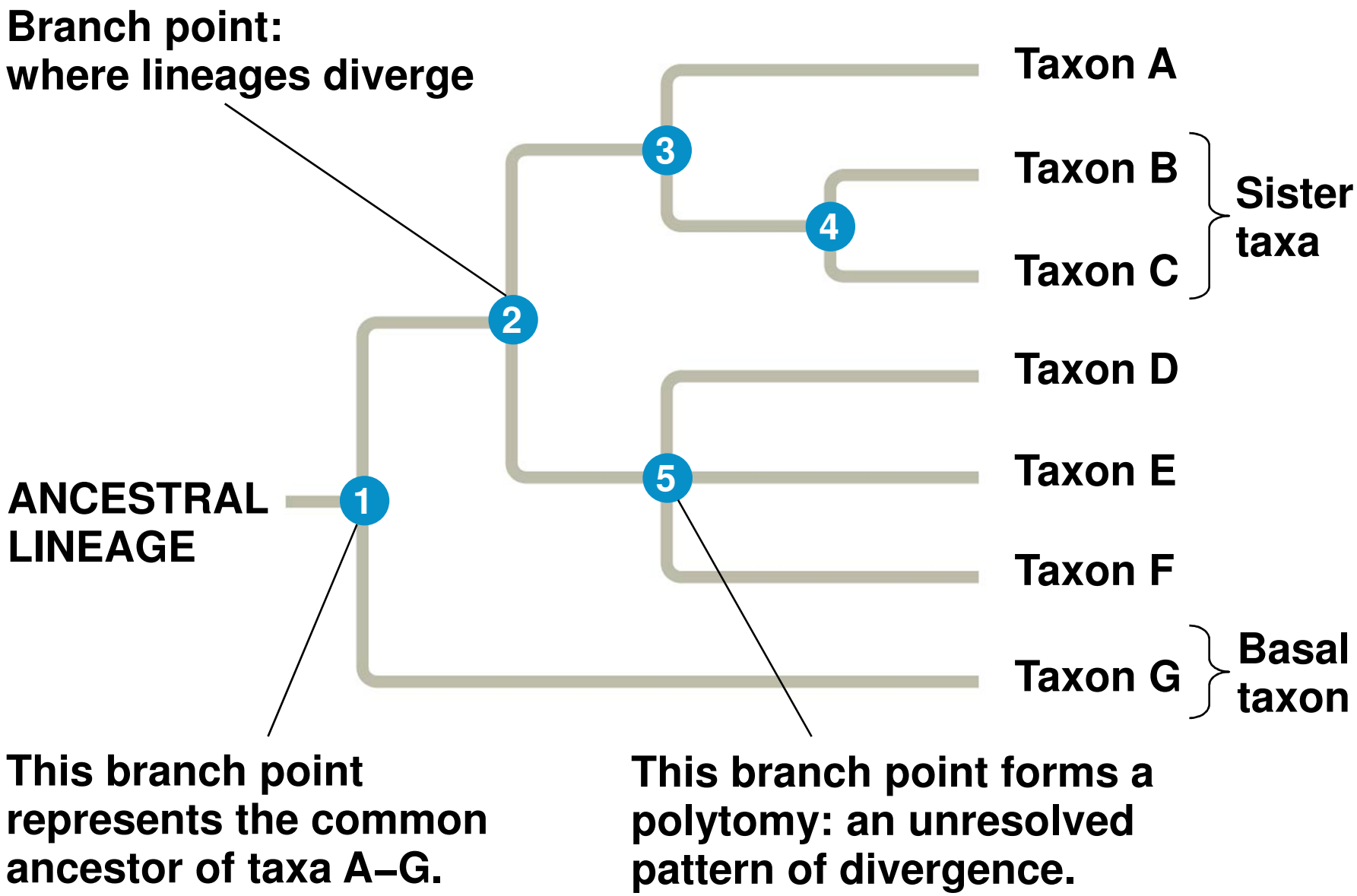

Order
Family
Genus
Species
Carnivora
Felidae
Mustelidae
Canidae
Panthera
Taxidea
Lutra
Canis
1
2
Panthera pardus (leopard)
Taxidea taxus (American badger)
Lutra lutra (European otter)
Canis latrans (coyote)
Canis lupus (gray wolf)

Figure 20.5


Branch point:
where lineages diverge
Taxon A
Taxon B
Taxon C
Sister taxa
Taxon D
Taxon E
Taxon F
Taxon G
Basal taxon
ANCESTRAL LINEAGE
1
2
3
4
5
This branch point represents the common ancestor of taxa A–G.
This branch point forms a polytomy: an unresolved pattern of divergence.

What We Can and Cannot Learn from Phylogenetic Trees

- Phylogenetic trees show patterns of descent, not phenotypic similarity
- Phylogenetic trees do not generally indicate when a species evolved or how much change occurred in a lineage
- It should not be assumed that a taxon evolved from the taxon next to it

Applying Phylogenies

- Phylogeny provides important information about similar characteristics in closely related species
  - May be useful in cross-breeding or genetic engineering
- Phylogenetic trees based on DNA sequences can be used to infer species identities
  - Useful in investigating poaching

Concept 20.2: Phylogenies are inferred from morphological and molecular data

- To infer phylogeny, systematists gather information about morphologies, genes, and biochemistry of living organisms
- The similarities used to infer phylogenies must result from shared ancestry

Morphological and Molecular Homologies

- Phenotypic and genetic similarities due to shared ancestry are called *homologies*
- Organisms with similar morphologies or DNA sequences are likely to be more closely related than organisms with different structures or sequences

Sorting Homology from Analogy

- When constructing a phylogeny, systematists need to distinguish whether a similarity is the result of homology or **analogy**
- Homology is similarity due to shared ancestry
  - Similar structure
- Analogy is similarity due to convergent evolution
  - Similar function
- Convergent evolution occurs when similar environmental pressures and natural selection produce similar (analogous) adaptations in organisms from different evolutionary lineages

Figure 20.7

- Bat and bird wings are homologous as forelimbs, but analogous as functional wings
- Analogous structures or molecular sequences that evolved independently are also called **homoplasies**
- Homology can be distinguished from analogy by comparing fossil evidence and the degree of complexity
- The more complex two similar structures are, the more likely it is that they are homologous
- If genes in two organisms share many portions of their nucleotide sequence, the genes are likely homologous

Evaluating Molecular Homologies

- Molecular homologies are determined based on the degree of similarity in nucleotide sequence between taxa
  - If species are very closely related, the sequences probably only differ in a few sites
  - Distantly related species usually have different bases at many sites and may have different lengths
- Systematists use computer programs when analyzing comparable DNA segments from different organisms

Concept 20.3: Shared characters are used to construct phylogenetic trees

- In reconstructing phylogenies, the first step is to distinguish homologous features from analogous ones
  - Remember, only homology reflects evolutionary history
- **Cladistics** classifies organisms by common descent
- A **clade** is a group of species that includes an ancestral species and all its descendants
  - Clades can be nested in larger clades, but not all groupings of organisms qualify as clades

Concept 20.4: Molecular clocks help track evolutionary time

- To extend molecular phylogenies beyond the fossil record, we must make an assumption about how molecular change occurs over time
- A **molecular clock** uses constant rates of evolution in some genes to estimate the absolute time of evolutionary change
- The number of nucleotide substitutions in related genes is assumed to be proportional to the time since they last shared a common ancestor

Concept 20.5: New information continues to revise our understanding of evolutionary history

- Recently, systematists have gained insight into the very deepest branches of the tree of life through analysis of DNA sequence data

From Two Kingdoms to Three Domains

- Early taxonomists classified all species as either plants or animals
- Later, five kingdoms were recognized: Monera (prokaryotes), Protista, Plantae, Fungi, and Animalia
- More recently, the three-domain system has been adopted: Bacteria, Archaea, and Eukarya
- The three-domain system is supported by data from many sequenced genomes

Figure 20.20a

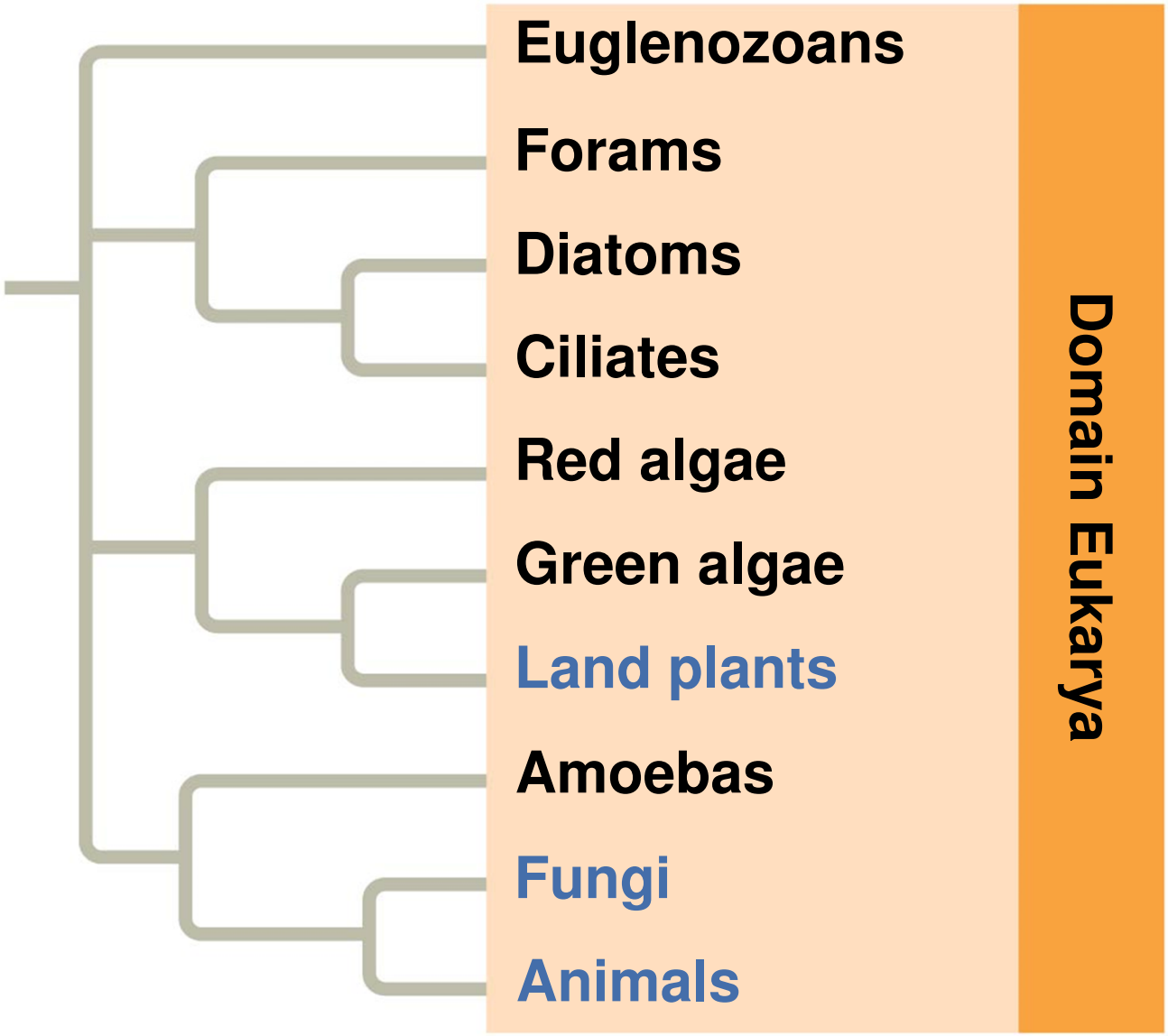


Figure 20.20b

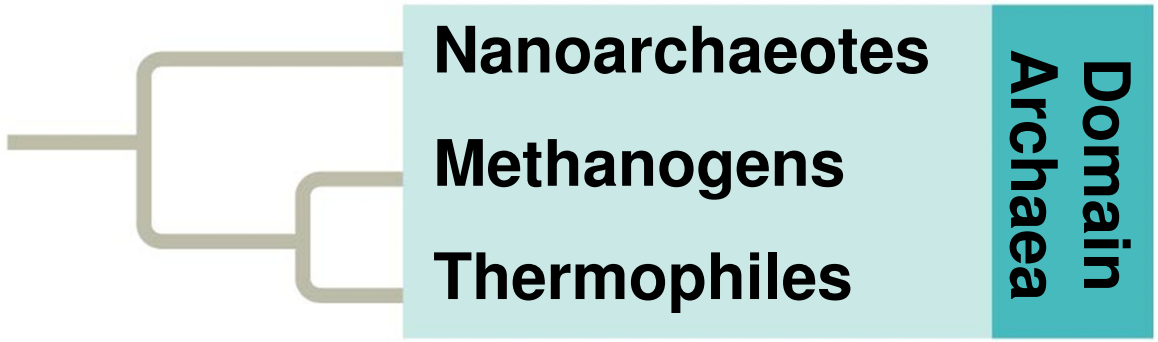
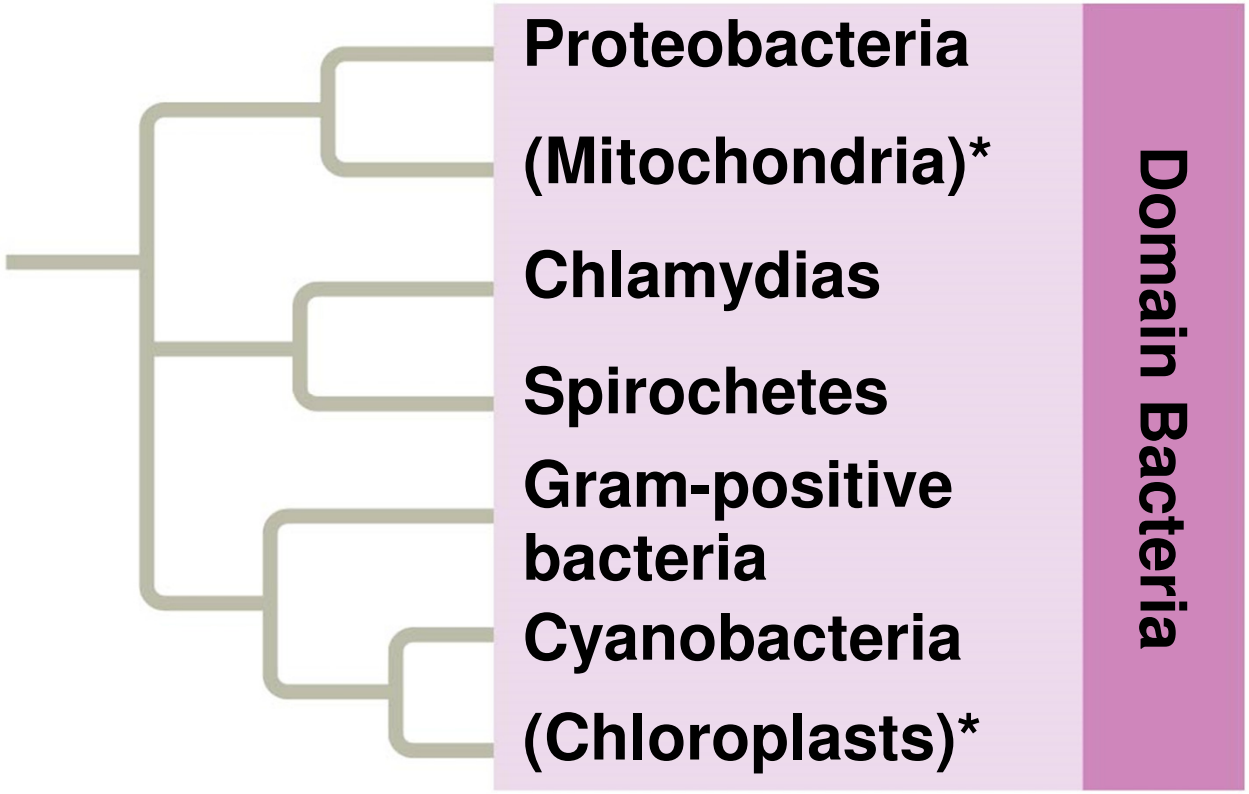


Figure 20.20c



- The three-domain system highlights the importance of single-celled organisms in the history of life
- Domains Bacteria and Archaea are single-celled prokaryotes
- Only three lineages in the domain Eukarya are dominated by multicellular organisms
  - Kingdoms Plantae, Fungi, and Animalia

The Important Role of Horizontal Gene Transfer

- There have been substantial interchanges of genes between organisms in different domains
- **Horizontal gene transfer** is the movement of genes from one genome to another
  - Occurs by exchange of transposable elements and plasmids, viral infection, and fusion of organisms
- Horizontal gene transfer complicates efforts to build a tree of life